

10/567749

SEQUENCE LISTING:

5 <110> Degussa AG

<120> Process for the preparation of L-threonine

10 <130> 030235 BT

<160> 10

<170> PatentIn version 3.1

15 <210> 1

<211> 993

<212> DNA

<213> Escherichia coli

20 <220>

<221> CDS

<222> (1)..(990)

<223> rpos gene

25 <400> 1

atg agt cag aat acg ctg aaa gtt cat gat tta aat gaa gat gcg gaa	48
Met Ser Gln Asn Thr Leu Lys Val His Asp Leu Asn Glu Asp Ala Glu	
1 5 10 15	
30 ttt gat gag aac gga gtt gag gtt ttt gac gaa aag gcc tta gta gaa	96
Phe Asp Glu Asn Gly Val Glu Val Phe Asp Glu Lys Ala Leu Val Glu	
20 25 30	
35 cag gaa ccc agt gat aac gat ttg gcc gaa gag gaa ctg tta tgc cag	144
Gln Glu Pro Ser Asp Asn Asp Leu Ala Glu Glu Glu Leu Leu Ser Gln	
35 40 45	
40 gga gcc aca cag cgt gtg ttg gac gcg act cag ctt tac ctt ggt gag	192
Gly Ala Thr Gln Arg Val Leu Asp Ala Thr Gln Leu Tyr Leu Gly Glu	
50 55 60	
45 att ggt tat tca cca ctg tta acg gcc gaa gaa gaa gtt tat ttt gcg	240
Ile Gly Tyr Ser Pro Leu Leu Thr Ala Glu Glu Glu Val Tyr Phe Ala	
65 70 75 80	
50 cgt cgc gca ctg cgt gga gat gtc gcc tct cgc cgc cgg atg atc gag	288
Arg Arg Ala Leu Arg Gly Asp Val Ala Ser Arg Arg Arg Met Ile Glu	
85 90 95	
55 agt aac ttg cgt ctg gtg gta aaa att gcc cgc cgt tat ggc aat cgt	336
Ser Asn Leu Arg Leu Val Val Lys Ile Ala Arg Arg Tyr Gly Asn Arg	
100 105 110	
55 ggt ctg gcg ttg ctg gac ctt atc gaa gag ggc aac ctg ggg ctg atc	384
Gly Leu Ala Leu Leu Asp Leu Ile Glu Glu Gly Asn Leu Gly Leu Ile	
115 120 125	
60 cgc gcg gta gag aag ttt gac ccg gaa cgt ggt ttc cgc ttc tca aca	432
Arg Ala Val Glu Lys Phe Asp Pro Glu Arg Gly Phe Arg Phe Ser Thr	
130 135 140	
65 tac gca acc tgg tgg att cgc cag acg att gaa cgg gcg att atg aac	480
Tyr Ala Thr Trp Trp Ile Arg Gln Thr Ile Glu Arg Ala Ile Met Asn	
145 150 155 160	

	caa acc cgt act att cgt ttg ccg att cac atc gta aag gag ctg aac	528
	Gln Thr Arg Thr Ile Arg Leu Pro Ile His Ile Val Lys Glu Leu Asn	
	165 170 175	
5	gtt tac ctg cga acc gca cgt gag ttg tcc cat aag ctg gac cat gaa	576
	Val Tyr Leu Arg Thr Ala Arg Glu Leu Ser His Lys Leu Asp His Glu	
	180 185 190	
10	cca agt gcg gaa gag atc gca gag caa ctg gat aag cca gtt gat gac	624
	Pro Ser Ala Glu Glu Ile Ala Glu Gln Leu Asp Lys Pro Val Asp Asp	
	195 200 205	
15	gtc agc cgt atg ctt cgt ctt aac gag cgc att acc tcg gta gac acc	672
	Val Ser Arg Met Leu Arg Leu Asn Glu Arg Ile Thr Ser Val Asp Thr	
	210 215 220	
20	ccg ctg ggt ggt gat tcc gaa aaa gcg ttg ctg gac atc ctg gcc gat	720
	Pro Leu Gly Gly Asp Ser Glu Lys Ala Leu Leu Asp Ile Leu Ala Asp	
	225 230 235 240	
	gaa aaa gag aac ggt ccg gaa gat acc acg caa gat gac gat atg aag	768
	Glu Lys Glu Asn Gly Pro Glu Asp Thr Thr Gln Asp Asp Asp Met Lys	
	245 250 255	
25	cag agc atc gtc aaa tgg ctg ttc gag ctg aac gcc aaa cag cgt gaa	816
	Gln Ser Ile Val Lys Trp Leu Phe Glu Leu Asn Ala Lys Gln Arg Glu	
	260 265 270	
30	gtg ctg gca cgt cga ttc ggt ttg ctg ggg tac gaa gcg gca aca ctg	864
	Val Leu Ala Arg Arg Phe Gly Leu Leu Gly Tyr Glu Ala Ala Thr Leu	
	275 280 285	
35	gaa gat gta ggt cgt gaa att ggc ctc acc cgt gaa cgt gtt cgc cag	912
	Glu Asp Val Gly Arg Glu Ile Gly Leu Thr Arg Glu Arg Val Arg Gln	
	290 295 300	
40	att cag gtt gaa ggc ctg cgc cgt ttg cgc gaa atc ctg caa acg cag	960
	Ile Gln Val Glu Gly Leu Arg Arg Leu Arg Glu Ile Leu Gln Thr Gln	
	305 310 315 320	
	ggg ctg aat atc gaa gcg ctg ttc cgc gag taa	993
	Gly Leu Asn Ile Glu Ala Leu Phe Arg Glu	
	325 330	
45	<210> 2	
	<211> 330	
	<212> PRT	
	<213> Escherichia coli	
50	<400> 2	
	Met Ser Gln Asn Thr Leu Lys Val His Asp Leu Asn Glu Asp Ala Glu	
	1 5 10 15	
55	Phe Asp Glu Asn Gly Val Glu Val Phe Asp Glu Lys Ala Leu Val Glu	
	20 25 30	
	Gln Glu Pro Ser Asp Asn Asp Leu Ala Glu Glu Glu Leu Leu Ser Gln	
	35 40 45	
60	Gly Ala Thr Gln Arg Val Leu Asp Ala Thr Gln Leu Tyr Leu Gly Glu	
	50 55 60	
65	Ile Gly Tyr Ser Pro Leu Leu Thr Ala Glu Glu Glu Val Tyr Phe Ala	
	65 70 75 80	

Arg Arg Ala Leu Arg Gly Asp Val Ala Ser Arg Arg Arg Met Ile Glu
 85 90 95
 5 Ser Asn Leu Arg Leu Val Val Lys Ile Ala Arg Arg Tyr Gly Asn Arg
 100 105 110
 Gly Leu Ala Leu Leu Asp Leu Ile Glu Glu Gly Asn Leu Gly Leu Ile
 115 120 125
 10 Arg Ala Val Glu Lys Phe Asp Pro Glu Arg Gly Phe Arg Phe Ser Thr
 130 135 140
 Tyr Ala Thr Trp Trp Ile Arg Gln Thr Ile Glu Arg Ala Ile Met Asn
 145 150 155 160
 15 Gln Thr Arg Thr Ile Arg Leu Pro Ile His Ile Val Lys Glu Leu Asn
 165 170 175
 Val Tyr Leu Arg Thr Ala Arg Glu Leu Ser His Lys Leu Asp His Glu
 180 185 190
 Pro Ser Ala Glu Glu Ile Ala Glu Gln Leu Asp Lys Pro Val Asp Asp
 195 200 205
 25 Val Ser Arg Met Leu Arg Leu Asn Glu Arg Ile Thr Ser Val Asp Thr
 210 215 220
 Pro Leu Gly Gly Asp Ser Glu Lys Ala Leu Leu Asp Ile Leu Ala Asp
 225 230 235 240
 30 Glu Lys Glu Asn Gly Pro Glu Asp Thr Thr Gln Asp Asp Asp Met Lys
 245 250 255
 Gln Ser Ile Val Lys Trp Leu Phe Glu Leu Asn Ala Lys Gln Arg Glu
 260 265 270
 Val Leu Ala Arg Arg Phe Gly Leu Leu Gly Tyr Glu Ala Ala Thr Leu
 275 280 285
 40 Glu Asp Val Gly Arg Glu Ile Gly Leu Thr Arg Glu Arg Val Arg Gln
 290 295 300
 Ile Gln Val Glu Gly Leu Arg Arg Leu Arg Glu Ile Leu Gln Thr Gln
 305 310 315 320
 45 Gly Leu Asn Ile Glu Ala Leu Phe Arg Glu
 325 330
 50 <210> 3
 <211> 993
 <212> DNA
 <213> Escherichia coli
 55 <220>
 <221> Allele
 <222> (1)..(990)
 <223> rpoS allele
 60 <220>
 <221> misc_feature
 <222> (97)..(99)
 <223> amber codon
 65 <400> 3
 atgagtcaga atacgctgaa agttcatgat ttaaataag atgcggaatt tgatgagaac 60

```

      ggagttgagg tttttgacga aaaggcctta gtagaatagg aaccagtgta taacgatttg      120
5    gccgaagagg aactgttata gcagggagcc acacagcgtg tgttggacgc gactcagctt      180
      taccttggtg agattggtta ttcaccactg ttaacggccg aagaagaagt ttattttgcg      240
      cgtcgcgcac tgcgtggaga tgtcgcctct cgccgccgga tgatcgagag taacttgcgt      300
10   ctggtggtaa aaattgcccc cggttatggc aatcgtggtc tggcgttgct ggaccttata      360
      gaagagggca acctggggct gatccgcgcg gtagagaagt ttgacccgga acgtggtttc      420
15   cgcttctcaa catacgcaac ctggtggatt cgccagacga ttgaacgggc gattatgaac      480
      caaaccgta ctattcgttt gccgattcac atcgtaaagg agctgaacgt ttacctgcga      540
      accgcacgtg agttgtccca taagctggac catgaaccaa gtgcggaaga gatcgagag      600
20   caactggata agccagttga tgacgtcagc cgtatgcttc gtcttaacga gcgcattacc      660
      tcggtagaca ccccgctggg tggtgattcc gaaaaagcgt tgctggacat cctggccgat      720
25   gaaaaagaga acggtccgga agataccacg caagatgacg atatgaagca gagcatcgtc      780
      aaatggctgt tcgagctgaa cgccaaacag cgtgaagtgc tggcacgtcg attcggtttg      840
      ctgggggtacg aagcggcaac actggaagat gtaggtcgtg aaattggcct caccctgtaa      900
30   cgtgttcgcc agattcaggt tgaaggcctg cgccgtttgc gcgaaatcct gcaaacgcag      960
      gggctgaata tcgaagcgtt gttccgcgag taa                                993

35   <210> 4
      <211> 75
      <212> DNA
      <213> Escherichia coli

40   <220>
      <221> tRNA
      <222> (1)..(75)
      <223> supE allele

45   <400> 4
      tggggtatcg ccaagcggta aggcaccgga ttctaattcc ggcattccga ggttcgaatc      60
      ctogtacccc agcca                                75

```

```

<210> 5
<211> 1545
<212> DNA
<213> Escherichia coli
5

<220>
<221> CDS
<222> (1)..(1542)
10 <223> ilvA-Gen

<400> 5
atg gct gac tcg caa ccc ctg tcc ggt gct ccg gaa ggt gcc gaa tat 48
Met Ala Asp Ser Gln Pro Leu Ser Gly Ala Pro Glu Gly Ala Glu Tyr
1 5 10 15

tta aga gca gtg ctg cgc gcg ccg gtt tac gag gcg gcg cag gtt acg 96
Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr
20 25 30

ccg cta caa aaa atg gaa aaa ctg tcg tcg cgt ctt gat aac gtc att 144
Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile
35 40 45

ctg gtg aag cgc gaa gat cgc cag cca gtg cac agc ttt aag ctg cgc 192
Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg
50 55 60

ggc gca tac gcc atg atg gcg ggc ctg acg gaa gaa cag aaa gcg cac 240
Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His
65 70 75 80

ggc gtg atc act gct tct gcg ggt aac cac gcg cag ggc gtc gcg ttt 288
Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe
85 90 95

tct tct gcg cgg tta ggc gtg aag gcc ctg atc gtt atg cca acc gcc 336
Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala
100 105 110

acc gcc gac atc aaa gtc gac gcg gtg cgc ggc ttc ggc ggc gaa gtg 384
Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val
115 120 125

ctg ctc cac ggc gcg aac ttt gat gaa gcg aaa gcc aaa gcg atc gaa 432
Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu
130 135 140

ctg tca cag cag cag ggg ttc acc tgg gtg ccg ccg ttc gac cat ccg 480
Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro
145 150 155 160

atg gtg att gcc ggg caa ggc acg ctg gcg ctg gaa ctg ctc cag cag 528
Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln
165 170 175

gac gcc cat ctc gac cgc gta ttt gtg cca gtc ggc ggc ggc ggt ctg 576
Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Gly Leu
180 185 190

gct gct ggc gtg gcg gtg ctg atc aaa caa ctg atg ccg caa atc aaa 624
Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys
195 200 205

```

	gtg	atc	gcc	gta	gaa	gcg	gaa	gac	tcc	gcc	tgc	ctg	aaa	gca	gcg	ctg	672
	Val	Ile	Ala	Val	Glu	Ala	Glu	Asp	Ser	Ala	Cys	Leu	Lys	Ala	Ala	Leu	
	210						215					220					
5	gat	gcg	ggt	cat	ccg	ggt	gat	ctg	ccg	cg	gta	ggg	cta	ttt	gct	gaa	720
	Asp	Ala	Gly	His	Pro	Val	Asp	Leu	Pro	Arg	Val	Gly	Leu	Phe	Ala	Glu	
	225					230					235					240	
10	ggc	gta	gcg	gta	aaa	cg	atc	ggt	gac	gaa	acc	ttc	cgt	tta	tgc	cag	768
	Gly	Val	Ala	Val	Lys	Arg	Ile	Gly	Asp	Glu	Thr	Phe	Arg	Leu	Cys	Gln	
					245					250					255		
15	gag	tat	ctc	gac	gac	atc	atc	acc	gtc	gat	agc	gat	gcg	atc	tgt	gcg	816
	Glu	Tyr	Leu	Asp	Asp	Ile	Ile	Thr	Val	Asp	Ser	Asp	Ala	Ile	Cys	Ala	
				260					265					270			
20	gcg	atg	aag	gat	tta	ttc	gaa	gat	gtg	cg	gcg	gtg	gcg	gaa	ccc	tct	864
	Ala	Met	Lys	Asp	Leu	Phe	Glu	Asp	Val	Arg	Ala	Val	Ala	Glu	Pro	Ser	
			275					280					285				
	ggc	gcg	ctg	gcg	ctg	gcg	gga	atg	aaa	aaa	tat	atc	gcc	ctg	cac	aac	912
	Gly	Ala	Leu	Ala	Leu	Ala	Gly	Met	Lys	Lys	Tyr	Ile	Ala	Leu	His	Asn	
		290					295					300					
25	att	cg	ggc	gaa	cg	ctg	gcg	cat	att	ctt	tcc	ggt	gcc	aac	gtg	aac	960
	Ile	Arg	Gly	Glu	Arg	Leu	Ala	His	Ile	Leu	Ser	Gly	Ala	Asn	Val	Asn	
	305					310					315					320	
30	ttc	cac	ggc	ctg	cg	tac	gtc	tca	gaa	cg	tgc	gaa	ctg	ggc	gaa	cag	1008
	Phe	His	Gly	Leu	Arg	Tyr	Val	Ser	Glu	Arg	Cys	Glu	Leu	Gly	Glu	Gln	
					325					330					335		
35	cgt	gaa	gcg	ttg	ttg	gcg	gtg	acc	att	ccg	gaa	gaa	aaa	ggc	agc	ttc	1056
	Arg	Glu	Ala	Leu	Leu	Ala	Val	Thr	Ile	Pro	Glu	Glu	Lys	Gly	Ser	Phe	
				340					345					350			
40	ctc	aaa	ttc	tgc	caa	ctg	ctt	ggc	ggg	cgt	tcg	gtc	acc	gag	ttc	aac	1104
	Leu	Lys	Phe	Cys	Gln	Leu	Leu	Gly	Gly	Arg	Ser	Val	Thr	Glu	Phe	Asn	
			355					360					365				
	tac	cgt	ttt	gcc	gat	gcc	aaa	aac	gcc	tgc	atc	ttt	gtc	ggt	gtg	cg	1152
	Tyr	Arg	Phe	Ala	Asp	Ala	Lys	Asn	Ala	Cys	Ile	Phe	Val	Gly	Val	Arg	
		370					375					380					
45	ctg	agc	cg	ggc	ctc	gaa	gag	cg	aaa	gaa	att	ttg	cag	atg	ctc	aac	1200
	Leu	Ser	Arg	Gly	Leu	Glu	Glu	Arg	Lys	Glu	Ile	Leu	Gln	Met	Leu	Asn	
	385					390					395					400	
50	gac	ggc	ggc	tac	agc	gtg	ggt	gat	ctc	tcc	gac	gac	gaa	atg	gcg	aag	1248
	Asp	Gly	Gly	Tyr	Ser	Val	Val	Asp	Leu	Ser	Asp	Asp	Glu	Met	Ala	Lys	
					405					410					415		
55	cta	cac	gtg	cg	tat	atg	gtc	ggc	gga	cgt	cca	tcg	cat	ccg	ttg	cag	1296
	Leu	His	Val	Arg	Tyr	Met	Val	Gly	Gly	Arg	Pro	Ser	His	Pro	Leu	Gln	
				420				425						430			
60	gaa	cg	ctc	tac	agc	ttc	gaa	ttc	ccg	gaa	tca	ccg	ggc	gcg	ctg	ctg	1344
	Glu	Arg	Leu	Tyr	Ser	Phe	Glu	Phe	Pro	Glu	Ser	Pro	Gly	Ala	Leu	Leu	
			435					440					445				
	cg	ttc	ctc	aac	acg	ctg	ggt	acg	tac	tgg	aac	att	tct	ttg	ttc	cac	1392
	Arg	Phe	Leu	Asn	Thr	Leu	Gly	Thr	Tyr	Trp	Asn	Ile	Ser	Leu	Phe	His	
		450					455					460					

	tat cgc agc cat ggc acc gac tac ggg cgc gta ctg gcg gcg ttc gaa	1440
	Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu	
	465 470 475 480	
5	ctt ggc gac cat gaa ccg gat ttc gaa acc cgg ctg aat gag ctg ggc	1488
	Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly	
	485 490 495	
10	tac gat tgc cac gac gaa acc aat aac ccg gcg ttc agg ttc ttt ttg	1536
	Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu	
	500 505 510	
15	gcg ggt tag	1545
	Ala Gly	
	<210> 6	
	<211> 514	
	<212> PRT	
20	<213> Escherichia coli	
	<400> 6	
25	Met Ala Asp Ser Gln Pro Leu Ser Gly Ala Pro Glu Gly Ala Glu Tyr	
	1 5 10 15	
	Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr	
	20 25 30	
30	Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile	
	35 40 45	
	Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg	
35	50 55 60	
	Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His	
	65 70 75 80	
40	Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe	
	85 90 95	
	Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala	
	100 105 110	
45	Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val	
	115 120 125	
	Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu	
50	130 135 140	
	Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro	
	145 150 155 160	
55	Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln	
	165 170 175	
	Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Gly Leu	
	180 185 190	
60	Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys	
	195 200 205	
65	Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu	
	210 215 220	

	Asp	Ala	Gly	His	Pro	Val	Asp	Leu	Pro	Arg	Val	Gly	Leu	Phe	Ala	Glu
	225					230					235					240
5	Gly	Val	Ala	Val	Lys	Arg	Ile	Gly	Asp	Glu	Thr	Phe	Arg	Leu	Cys	Gln
					245					250					255	
	Glu	Tyr	Leu	Asp	Asp	Ile	Ile	Thr	Val	Asp	Ser	Asp	Ala	Ile	Cys	Ala
				260					265					270		
10	Ala	Met	Lys	Asp	Leu	Phe	Glu	Asp	Val	Arg	Ala	Val	Ala	Glu	Pro	Ser
			275					280					285			
	Gly	Ala	Leu	Ala	Leu	Ala	Gly	Met	Lys	Lys	Tyr	Ile	Ala	Leu	His	Asn
15		290					295					300				
	Ile	Arg	Gly	Glu	Arg	Leu	Ala	His	Ile	Leu	Ser	Gly	Ala	Asn	Val	Asn
	305					310					315					320
	Phe	His	Gly	Leu	Arg	Tyr	Val	Ser	Glu	Arg	Cys	Glu	Leu	Gly	Glu	Gln
20					325					330					335	
	Arg	Glu	Ala	Leu	Leu	Ala	Val	Thr	Ile	Pro	Glu	Glu	Lys	Gly	Ser	Phe
				340					345					350		
25	Leu	Lys	Phe	Cys	Gln	Leu	Leu	Gly	Gly	Arg	Ser	Val	Thr	Glu	Phe	Asn
			355					360					365			
	Tyr	Arg	Phe	Ala	Asp	Ala	Lys	Asn	Ala	Cys	Ile	Phe	Val	Gly	Val	Arg
30		370					375					380				
	Leu	Ser	Arg	Gly	Leu	Glu	Glu	Arg	Lys	Glu	Ile	Leu	Gln	Met	Leu	Asn
	385					390					395					400
	Asp	Gly	Gly	Tyr	Ser	Val	Val	Asp	Leu	Ser	Asp	Asp	Glu	Met	Ala	Lys
35					405					410					415	
	Leu	His	Val	Arg	Tyr	Met	Val	Gly	Gly	Arg	Pro	Ser	His	Pro	Leu	Gln
				420					425					430		
40	Glu	Arg	Leu	Tyr	Ser	Phe	Glu	Phe	Pro	Glu	Ser	Pro	Gly	Ala	Leu	Leu
			435					440					445			
	Arg	Phe	Leu	Asn	Thr	Leu	Gly	Thr	Tyr	Trp	Asn	Ile	Ser	Leu	Phe	His
45		450					455					460				
	Tyr	Arg	Ser	His	Gly	Thr	Asp	Tyr	Gly	Arg	Val	Leu	Ala	Ala	Phe	Glu
	465					470					475					480
	Leu	Gly	Asp	His	Glu	Pro	Asp	Phe	Glu	Thr	Arg	Leu	Asn	Glu	Leu	Gly
50					485					490					495	
	Tyr	Asp	Cys	His	Asp	Glu	Thr	Asn	Asn	Pro	Ala	Phe	Arg	Phe	Phe	Leu
				500					505					510		
55	Ala	Gly														

	<210>	7
	<211>	1545
60	<212>	DNA
	<213>	Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1542)
 <223> ilvA-Allel

5

<220>
 <221> mutation
 <222> (856)..(856)
 <223>

10

<400> 7

15	atg gct gac tcg caa ccc ctg tcc ggt gct ccg gaa ggt gcc gaa tat	48
	Met Ala Asp Ser Gln Pro Leu Ser Gly Ala Pro Glu Gly Ala Glu Tyr	
	1 5 10 15	
20	tta aga gca gtg ctg cgc gcg ccg gtt tac gag gcg gcg cag gtt acg	96
	Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr	
	20 25 30	
25	ccg cta caa aaa atg gaa aaa ctg tcg tcg cgt ctt gat aac gtc att	144
	Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile	
	35 40 45	
30	ctg gtg aag cgc gaa gat cgc cag cca gtg cac agc ttt aag ctg cgc	192
	Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg	
	50 55 60	
35	ggc gca tac gcc atg atg gcg ggc ctg acg gaa gaa cag aaa gcg cac	240
	Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His	
	65 70 75 80	
40	ggc gtg atc act gct tct gcg ggt aac cac gcg cag ggc gtc gcg ttt	288
	Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe	
	85 90 95	
45	tct tct gcg cgg tta ggc gtg aag gcc ctg atc gtt atg cca acc gcc	336
	Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala	
	100 105 110	
50	acc gcc gac atc aaa gtc gac gcg gtg cgc ggc ttc ggc ggc gaa gtg	384
	Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val	
	115 120 125	
55	ctg ctc cac ggc gcg aac ttt gat gaa gcg aaa gcc aaa gcg atc gaa	432
	Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu	
	130 135 140	
60	ctg tca cag cag cag ggg ttc acc tgg gtg ccg ccg ttc gac cat ccg	480
	Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro	
	145 150 155 160	
65	atg gtg att gcc ggg caa ggc acg ctg gcg ctg gaa ctg ctc cag cag	528
	Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln	
	165 170 175	
70	gac gcc cat ctc gac cgc gta ttt gtg cca gtc ggc ggc ggc ggt ctg	576
	Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Gly Leu	
	180 185 190	
75	gct gct ggc gtg gcg gtg ctg atc aaa caa ctg atg ccg caa atc aaa	624
	Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys	
	195 200 205	

	gtg atc gcc gta gaa gcg gaa gac tcc gcc tgc ctg aaa gca gcg ctg	672
	Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu	
	210 215 220	
5	gat gcg ggt cat ccg gtt gat ctg ccg cgc gta ggg cta ttt gct gaa	720
	Asp Ala Gly His Pro Val Asp Leu Pro Arg Val Gly Leu Phe Ala Glu	
	225 230 235 240	
10	ggc gta gcg gta aaa cgc atc ggt gac gaa acc ttc cgt tta tgc cag	768
	Gly Val Ala Val Lys Arg Ile Gly Asp Glu Thr Phe Arg Leu Cys Gln	
	245 250 255	
15	gag tat ctc gac gac atc atc acc gtc gat agc gat gcg atc tgt gcg	816
	Glu Tyr Leu Asp Asp Ile Ile Thr Val Asp Ser Asp Ala Ile Cys Ala	
	260 265 270	
20	gcg atg aag gat tta ttc gaa gat gtg cgc gcg gtg gcg aaa ccc tct	864
	Ala Met Lys Asp Leu Phe Glu Asp Val Arg Ala Val Ala Lys Pro Ser	
	275 280 285	
	ggc gcg ctg gcg ctg gcg gga atg aaa aaa tat atc gcc ctg cac aac	912
	Gly Ala Leu Ala Leu Ala Gly Met Lys Lys Tyr Ile Ala Leu His Asn	
	290 295 300	
25	att cgc ggc gaa cgg ctg gcg cat att ctt tcc ggt gcc aac gtg aac	960
	Ile Arg Gly Glu Arg Leu Ala His Ile Leu Ser Gly Ala Asn Val Asn	
	305 310 315 320	
30	ttc cac ggc ctg cgc tac gtc tca gaa cgc tgc gaa ctg ggc gaa cag	1008
	Phe His Gly Leu Arg Tyr Val Ser Glu Arg Cys Glu Leu Gly Glu Gln	
	325 330 335	
35	cgt gaa gcg ttg ttg gcg gtg acc att ccg gaa gaa aaa ggc agc ttc	1056
	Arg Glu Ala Leu Leu Ala Val Thr Ile Pro Glu Glu Lys Gly Ser Phe	
	340 345 350	
40	ctc aaa ttc tgc caa ctg ctt ggc ggg cgt tgc gtc acc gag ttc aac	1104
	Leu Lys Phe Cys Gln Leu Leu Gly Gly Arg Ser Val Thr Glu Phe Asn	
	355 360 365	
	tac cgt ttt gcc gat gcc aaa aac gcc tgc atc ttt gtc ggt gtg cgc	1152
	Tyr Arg Phe Ala Asp Ala Lys Asn Ala Cys Ile Phe Val Gly Val Arg	
	370 375 380	
45	ctg agc cgc ggc ctc gaa gag cgc aaa gaa att ttg cag atg ctc aac	1200
	Leu Ser Arg Gly Leu Glu Glu Arg Lys Glu Ile Leu Gln Met Leu Asn	
	385 390 395 400	
50	gac ggc ggc tac agc gtg gtt gat ctc tcc gac gac gaa atg gcg aag	1248
	Asp Gly Gly Tyr Ser Val Val Asp Leu Ser Asp Asp Glu Met Ala Lys	
	405 410 415	
55	cta cac gtg cgc tat atg gtc ggc gga cgt cca tgc cat ccg ttg cag	1296
	Leu His Val Arg Tyr Met Val Gly Gly Arg Pro Ser His Pro Leu Gln	
	420 425 430	
60	gaa cgc ctc tac agc ttc gaa ttc ccg gaa tca ccg ggc gcg ctg ctg	1344
	Glu Arg Leu Tyr Ser Phe Glu Phe Pro Glu Ser Pro Gly Ala Leu Leu	
	435 440 445	
	cgc ttc ctc aac acg ctg ggt acg tac tgg aac att tct ttg ttc cac	1392
	Arg Phe Leu Asn Thr Leu Gly Thr Tyr Trp Asn Ile Ser Leu Phe His	
	450 455 460	

	tat cgc agc cat ggc acc gac tac ggg cgc gta ctg gcg gcg ttc gaa	1440
	Tyr Arg Ser His Gly Thr Asp Tyr Gly Arg Val Leu Ala Ala Phe Glu	
	465 470 475 480	
5	ctt ggc gac cat gaa ccg gat ttc gaa acc cgg ctg aat gag ctg ggc	1488
	Leu Gly Asp His Glu Pro Asp Phe Glu Thr Arg Leu Asn Glu Leu Gly	
	485 490 495	
10	tac gat tgc cac gac gaa acc aat aac ccg gcg ttc agg ttc ttt ttg	1536
	Tyr Asp Cys His Asp Glu Thr Asn Asn Pro Ala Phe Arg Phe Phe Leu	
	500 505 510	
15	gcg ggt tag	1545
	Ala Gly	
	<210> 8	
	<211> 514	
	<212> PRT	
20	<213> Escherichia coli	
	<400> 8	
25	Met Ala Asp Ser Gln Pro Leu Ser Gly Ala Pro Glu Gly Ala Glu Tyr	
	1 5 10 15	
	Leu Arg Ala Val Leu Arg Ala Pro Val Tyr Glu Ala Ala Gln Val Thr	
	20 25 30	
30	Pro Leu Gln Lys Met Glu Lys Leu Ser Ser Arg Leu Asp Asn Val Ile	
	35 40 45	
35	Leu Val Lys Arg Glu Asp Arg Gln Pro Val His Ser Phe Lys Leu Arg	
	50 55 60	
	Gly Ala Tyr Ala Met Met Ala Gly Leu Thr Glu Glu Gln Lys Ala His	
	65 70 75 80	
40	Gly Val Ile Thr Ala Ser Ala Gly Asn His Ala Gln Gly Val Ala Phe	
	85 90 95	
	Ser Ser Ala Arg Leu Gly Val Lys Ala Leu Ile Val Met Pro Thr Ala	
	100 105 110	
45	Thr Ala Asp Ile Lys Val Asp Ala Val Arg Gly Phe Gly Gly Glu Val	
	115 120 125	
50	Leu Leu His Gly Ala Asn Phe Asp Glu Ala Lys Ala Lys Ala Ile Glu	
	130 135 140	
	Leu Ser Gln Gln Gln Gly Phe Thr Trp Val Pro Pro Phe Asp His Pro	
	145 150 155 160	
55	Met Val Ile Ala Gly Gln Gly Thr Leu Ala Leu Glu Leu Leu Gln Gln	
	165 170 175	
	Asp Ala His Leu Asp Arg Val Phe Val Pro Val Gly Gly Gly Gly Leu	
	180 185 190	
60	Ala Ala Gly Val Ala Val Leu Ile Lys Gln Leu Met Pro Gln Ile Lys	
	195 200 205	
65	Val Ile Ala Val Glu Ala Glu Asp Ser Ala Cys Leu Lys Ala Ala Leu	
	210 215 220	

[illegible]

```

<220>
<221> DNA
<222> (1)..(1548)
<223>
5

<220>
<221> CDS
<222> (527)..(952)
10 <223> yjgF-Orf

<400> 9
15 tcgcgatctg gtactgtaag gggaaataga gatgacacac gataataaat tgcaggttga 60
agctattaaa cgcggcacgg taattgacca tatccccgcc cagatcggtt ttaagctggt 120
gagtctgttc aagctgaccg aaacggatca gcgcattcacc attggtctga acctgccttc 180
20 tggcgagatg ggccgcaaag atctgatcaa aatcgaaaat accttttttga gtgaagatca 240
agtagatcaa ctggcattgt atgcgccgca agccacgggt aaccgtatcg acaactatga 300
agtggtgggt aaatcgcgcc caagtctgcc ggagcgcac gacaatgtgc tggctctgccc 360
25 gaacagcaac tgtatcagcc atgccgaacc ggtttcatcc agctttgccc tgcgaaaacg 420
cgccaatgat atcgcgctca aatgcaaata ctgtgaaaaa gagttttccc ataatgtggt 480
30 gctggccaat taattgcggt tggttaataaa agtctggctc cctata atg agc cag 535
Met Ser Gln
1

act ttt tac cgc tgt aat aaa gga gaa atc atg agc aaa act atc gcg 583
35 Thr Phe Tyr Arg Cys Asn Lys Gly Glu Ile Met Ser Lys Thr Ile Ala
5 10 15

acg gaa aat gca ccg gca gct atc ggt cct tac gta cag ggc gtt gat 631
40 Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr Val Gln Gly Val Asp
20 25 30 35

ctg ggc aat atg atc atc acc tcc ggt cag atc ccg gta aat ccg aaa 679
Leu Gly Asn Met Ile Ile Thr Ser Gly Gln Ile Pro Val Asn Pro Lys
40 45 50

acg ggc gaa gta ccg gca gac gtc gct gca cag gca cgt cag tcg ctg 727
45 Thr Gly Glu Val Pro Ala Asp Val Ala Ala Gln Ala Arg Gln Ser Leu
55 60 65

gat aac gta aaa gcg atc gtc gaa gcc gct ggc ctg aaa gtg ggc gac 775
50 Asp Asn Val Lys Ala Ile Val Glu Ala Ala Gly Leu Lys Val Gly Asp
70 75 80

atc gtt aaa act acc gtg ttt gta aaa gat ctg aac gac ttc gca acc 823
55 Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu Asn Asp Phe Ala Thr
85 90 95

gta aac gcc act tac gaa gcc ttc ttc acc gaa cac aac gcc acc ttc 871
60 Val Asn Ala Thr Tyr Glu Ala Phe Phe Thr Glu His Asn Ala Thr Phe
100 105 110 115

ccg gca cgt tct tgc gtt gaa gtt gcc cgt ctg ccg aaa gac gtg aag 919
Pro Ala Arg Ser Cys Val Glu Val Ala Arg Leu Pro Lys Asp Val Lys
120 125 130
65

```

```

att gag atc gaa gcg atc gct gtt cgt cgc taa tcttgatgga aatccgggct 972
Ile Glu Ile Glu Ala Ile Ala Val Arg Arg
      135                      140

5  atcatgcccg gattaagtct gatgacaaac gcaaaatcgc ctgatgcgct acgcttatca 1032
   ggcctacgtg attcctgcaa tttattgaat ttgttggccg gataaggcat ttacgccgca 1092
   tccggcatga acaaaactca ctttgtctac aatctgaatc ggggctatcg tgcccagttt 1152
10 attctttatt gccagccgta acgacggcta tagaaccctt tcaccaactg ggttaatgtc 1212
   atataccctg ccagaatcgc aaccagccac gggaaatagc ttaacggcag cgcttgtaat 1272
15 tgcagataac tggccagcgg tgaaaacggc aatgcgatcc cgacaatcat cacgatcacg 1332
   gtcatgatca ttaacggcca cgatgcacag ctctgaataa acggcacacg gcgggtgcgg 1392
   atcatatgca caatcagcgt ttgcgacagt aagcccacca caaaccatcc cgactggaac 1452
20 agcgtttgcg tttccggcgt gttggcatgg aatacccacc acatcaggca aaacgtcaaa 1512
   atatcgaaga tcgagctgat cgggccgaag aagatc 1548

25
   <210> 10
   <211> 141
   <212> PRT
   <213> Escherichia coli
30

   <400> 10
   Met Ser Gln Thr Phe Tyr Arg Cys Asn Lys Gly Glu Ile Met Ser Lys
   1          5          10          15
35   Thr Ile Ala Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr Val Gln
      20          25          30
40   Gly Val Asp Leu Gly Asn Met Ile Ile Thr Ser Gly Gln Ile Pro Val
      35          40          45
      Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Val Ala Ala Gln Ala Arg
      50          55          60
45   Gln Ser Leu Asp Asn Val Lys Ala Ile Val Glu Ala Ala Gly Leu Lys
      65          70          75          80
      Val Gly Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu Asn Asp
      85          90          95
50   Phe Ala Thr Val Asn Ala Thr Tyr Glu Ala Phe Phe Thr Glu His Asn
      100          105          110
      Ala Thr Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg Leu Pro Lys
      115          120          125
55   Asp Val Lys Ile Glu Ile Glu Ala Ile Ala Val Arg Arg
      130          135          140

60

```